

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Conkling, Mark A.
Mendu, Nandini
Song, Wen

(ii) TITLE OF INVENTION: Regulation of Quinolate Phosphoribosyl Transferase Expression

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Kenneth Sibley, Bell Seltzer Park & Gibson
(B) STREET: Post Office Drawer 34009
(C) CITY: Charlotte
(D) STATE: North Carolina
(E) COUNTRY: USA
(F) ZIP: 28234

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sibley, Kenneth D.
(B) REGISTRATION NUMBER: 31,665
(C) REFERENCE/DOCKET NUMBER: 5051-338P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 919-420-2200
(B) TELEFAX: 919-881-3175

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 52..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAAAACTAT	TTTCCACAAA	ATTCATTC	CAACCCCC	AAAAAAAAC	C	ATG	TTT	57								
						Met	Phe									
							1									
AGA	GCT	ATT	CCT	TTC	ACT	GCT	ACA	GCT	105							
Arg	Ala	Ile	Pro	Phe	Thr	Ala	Thr	Val								
5								15								
CCA	AGG	TTG	GTG	GTG	AAA	ATG	TCA	GCA	ATA	GCC	ACC	AAG	AAT	ACA	AGA	153
Pro	Arg	Leu	Val	Val	Lys	Met	Ser	Ala	Ile	Ala	Thr	Lys	Asn	Thr	Arg	
20									25			30				
GTG	GAG	TCA	TTA	GAG	GTG	AAA	CCA	CCA	GCA	CAC	CCA	ACT	TAT	GAT	TTA	201
Val	Glu	Ser	Leu	Glu	Val	Lys	Pro	Pro	Ala	His	Pro	Thr	Tyr	Asp	Leu	
35									40			45			50	
AAG	GAA	GTT	ATG	AAA	CTT	GCA	CTC	TCT	GAA	GAT	GCT	GGG	AAT	TTA	GGA	249
Lys	Glu	Val	Met	Lys	Leu	Ala	Leu	Ser	Glu	Asp	Ala	Gly	Asn	Leu	Gly	
55									60			65				
GAT	GTG	ACT	TGT	AAG	GCG	ACA	ATT	CCT	CTT	GAT	ATG	GAA	TCC	GAT	GCT	297
Asp	Val	Thr	Cys	Lys	Ala	Thr	Ile	Pro	Leu	Asp	Met	Glu	Ser	Asp	Ala	
70									75			80				
CAT	TTT	CTA	GCA	AAG	GAA	GAC	GGG	ATC	ATA	GCA	GGA	ATT	GCA	CTT	GCT	345
His	Phe	Leu	Ala	Lys	Glu	Asp	Gly	Ile	Ile	Ala	Gly	Ile	Ala	Leu	Ala	
85									90			95				
GAG	ATG	ATA	TTC	GCG	GAA	GTT	GAT	CCT	TCA	TTA	AAG	GTG	GAG	TGG	TAT	393
Glu	Met	Ile	Phe	Ala	Glu	Val	Asp	Pro	Ser	Leu	Lys	Val	Glu	Trp	Tyr	
100									105			110				
GTA	AAT	GAT	GGC	GAT	AAA	GTT	CAT	AAA	GGC	TTG	AAA	TTT	GGC	AAA	GTA	441
Val	Asn	Asp	Gly	Asp	Lys	Val	His	Lys	Gly	Leu	Lys	Phe	Gly	Lys	Val	
115									120			125			130	
CAA	GGA	AAC	GCT	TAC	AAC	ATT	GTT	ATA	GCT	GAG	AGG	GTT	CTC	AAT	489	
Gln	Gly	Asn	Ala	Tyr	Asn	Ile	Val	Ile	Ala	Glu	Arg	Val	Val	Leu	Asn	
135									140			145				
TTT	ATG	CAA	AGA	ATG	AGT	GGA	ATA	GCT	ACA	CTA	ACT	AAG	GAA	ATG	GCA	537
Phe	Met	Gln	Arg	Met	Ser	Gly	Ile	Ala	Thr	Leu	Thr	Lys	Glu	Met	Ala	
150									155			160				
GAT	GCT	GCA	CAC	CCT	GCT	TAC	ATC	TTG	GAG	ACT	AGG	AAA	ACT	GCT	CCT	585
Asp	Ala	Ala	His	Pro	Ala	Tyr	Ile	Leu	Glu	Thr	Arg	Lys	Thr	Ala	Pro	
165									170			175				

GGA TTA CGT TTG GTG GAT AAA TGG GCG GTA TTG ATC GGT GGG GGG AAG Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Lys 180 185 190	633
AAT CAC AGA ATG GGC TTA TTT GAT ATG GTA ATG ATA AAA GAC AAT CAC Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His 195 200 205 210	681
ATA TCT GCT GGA GGT GTC GGC AAA GCT CTA AAA TCT GTG GAT CAG Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln 215 220 225	729
TAT TTG GAG CAA AAT AAA CTT CAA ATA GGG GTT GAG GTT GAA ACC AGG Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg 230 235 240	777
ACA ATT GAA GAA GTA CGT GAG GTT CTA GAC TAT GCA TCT CAA ACA AAG Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys 245 250 255	825
ACT TCG TTG ACT AGG ATA ATG CTG GAC AAT ATG GTT GTT CCA TTA TCT Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser 260 265 270	873
AAC GGA GAT ATT GAT GTA TCC ATG CTT AAG GAG GCT GTA GAA TTG ATC Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile 275 280 285 290	921
AAT GGG AGG TTT GAT ACG GAG GCT TCA GGA AAT GTT ACC CTT GAA ACA Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr 295 300 305	969
GTA CAC AAG ATT GGA CAA ACT GGT GTT ACC TAC ATT TCT AGT GGT GCC Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala 310 315 320	1017
CTG ACG CAT TCC GTG AAA GCA CTT GAC ATT TCC CTG AAG ATC GAT ACA Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr 325 330 335	1065
GAG CTC GCC CTT GAA GTT GGA AGG CGT ACA AAA CGA GCA TGAGCGCCAT Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala 340 345 350	1114
TACTTCTGCT ATAGGGTTGG AGTAAAAGCA GCTGAATAGC TGAAAGGTGC AAATAAGAAT	1174
CATTTTACTA GTTGTCAAAC AAAAGATCCT TCACTGTGTA ATCAAACAAA AAGATGTAAA	1234
TTGCTGGAAT ATCTCAGATG GCTCTTTCC AACCTTATTG CTTGAGTTGG TAATTTCATT	1294
ATAGCTTTGT TTTCATGTTT CATGGAATTT GTTACAATGA AAATACTTGA TTTATAAGTT	1354
TGGTGTATGT AAAATTCTGT GTTACTTCAA ATATTTGAG ATGTT	1399

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile
1 5 10 15

Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn
20 25 30

Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr
35 40 45

Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn
50 55 60

Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser
65 70 75 80

Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala
85 90 95

Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu
100 105 110

Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly
115 120 125

Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val
130 135 140

Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu
145 150 155 160

Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr
165 170 175

Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly
180 185 190

Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp
195 200 205

Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val
210 215 220

Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu
225 230 235 240

Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln
 245 250 255

Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro
 260 265 270

Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu
 275 280 285

Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu
 290 295 300

Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser
 305 310 315 320

Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile
 325 330 335

Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
 340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGTTTAGAG	CTATTCCTTT	CACTGCTACA	GTGCATCCTT	ATGCAATTAC	AGCTCCAAGG	60
TTGGTGGTGA	AAATGTCAGC	AATAGCCACC	AAGAATACAA	GAGTGGAGTC	ATTAGAGGTG	120
AAACCACCA	CACACCCAAAC	TTATGATT	AAGGAAGTTA	TGAAACTTGC	ACTCTCTGAA	180
GATGCTGGGA	ATTTAGGAGA	TGTGACTTGT	AAGGCGACAA	TTCCTCTTGA	TATGGAATCC	240
GATGCTCATT	TTCTAGCAAA	GGAAGACGGG	ATCATAGCAG	GAATTGCAGT	TGCTGAGATG	300
ATATTCGCGG	AAGTTGATCC	TTCATTAAAG	GTGGAGTGGT	ATGTAAATGA	TGGCGATAAA	360
GTTCATAAAG	GCTTGAAATT	TGGCAAAGTA	CAAGGAAACG	CTTACAACAT	TGTTATAGCT	420
GAGAGGGTTG	TTCTCAATT	TATGCAAAGA	ATGAGTGGAA	TAGCTACACT	AACTAAGGAA	480
ATGGCAGATG	CTGCACACCC	TGCTTACATC	TTGGAGACTA	GGAAAATGTC	TCCTGGATT	540
CGTTTGGTGG	ATAAATGGGC	GGTATTGATC	GGTGGGGGGA	AGAATCACAG	AATGGGCTTA	600

TTTGATATGG TAATGATAAA AGACAATCAC ATATCTGCTG CTGGAGGTGT CGGCAAAGCT	660
CTAAAATCTG TGGATCAGTA TTTGGAGCAA AATAAACTTC AAATAGGGGT TGAGGTTGAA	720
ACCAGGACAA TTGAAGAAGT ACGTGAGGTT CTAGACTATG CATCTCAAAC AAAGACTTCG	780
TTGACTAGGA TAATGCTGGA CAATATGGTT GTTCCATTAT CTAACGGAGA TATTGATGTA	840
TCCATGCTTA AGGAGGCTGT AGAATTGATC AATGGGAGGT TTGATAACGGA GGCTTCAGGA	900
AATGTTACCC TTGAAACAGT ACACAAGATT GGACAAACTG GTGTTACCTA CATTCTAGT	960
GGTGCCCTGA CGCATTCCGT GAAAGCACTT GACATTTCCC TGAAGATCGA TACAGAGCTC	1020
GCCCTTGAAAG TTGGAAGGCG TACAAAACGA GCA	1053